

JAYPEE UNIVERSITY OF INFORMATION TECHNOLOGY, WAKNAGHAT

TEST -1 EXAMINATION- 2023

B.Tech-I Semester (CSE/IT/ECE/CE)

COURSE CODE(CREDITS): 18B11BI313(4)

MAX. MARKS: 15

COURSE NAME: Biological Computation

COURSE INSTRUCTORS: Dr. Shikha Mittal

MAX. TIME: 1 Hour

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*Note: (a) All questions are compulsory.*

*(b) Marks are indicated against each question in square brackets.*

*(c) The candidate is allowed to make Suitable numeric assumptions wherever required for solving problems*

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Q1. Define BLAST, it's variants and also explain the BLAST algorithm using a flow chart.

(CO-1) [3]

Q2. Consecute the global alignment for the given sequences considering match = 1, mismatch = 0 and gap = -1

(CO-2) [4]

Seq1 - ACAA

Seq2 - ACTGA

Q3. Briefly explain sequence alignment and methods used for sequence alignment.

(CO-2) [2]

Q4. What are the substitution or scoring matrices used for sequence alignment of amino acids and also list 3 differences between them.

(CO-2) [3]

Q5. Explain the following

(CO-1) [3]

- A. Orthologs, Paralogs and Homologs
- B. E-value and bits code in BLAST
- C. Affine gap penalty